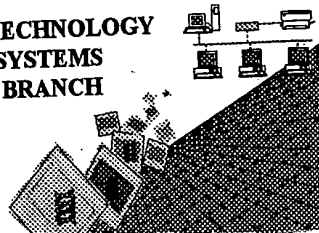


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0570  
0730

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/821,782B  
Source: OPE  
Date Processed by STIC: 8/8/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

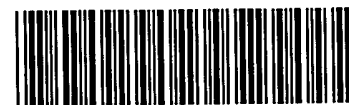
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



Does Not Comply  
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/821,782B

DATE: 08/08/2002  
TIME: 12:08:11

Errors throughout.  
See also pp 6 + 7 for  
additional errors.

Input Set : A:\0133659 sequence listing.txt  
Output Set: N:\CRF4\08082002\I821782B.raw

4 <110> APPLICANT: Kumar Verma, Sunil  
5 Singh, Lalji  
7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION  
9 <130> FILE REFERENCE: U-013365-9  
11 <140> CURRENT APPLICATION NUMBER: 09/821782B  
13 <141> CURRENT FILING DATE: 2001-03-29  
15 <160> NUMBER OF SEQ ID NOS: 255

#### ERRORED SEQUENCES

17 <210> SEQ ID NO: 1  
19 <211> LENGTH: (25) - Counted 26  
21 <212> TYPE: DNA  
23 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
27 <223> OTHER INFORMATION: Universal primer "mcb 398" for amplifying fragment of  
cytochrome b gene

28 of animal species  
30 <400> SEQUENCE: 1

E--> 32 taccatgagg acaaatatcta ttctg

(25) - Counted  
26

412 <210> SEQ ID NO: 19

414 <211> LENGTH: (328) - found 327

416 <212> TYPE: DNA

418 <213> ORGANISM: gz21CL

420 <220> FEATURE:

422 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard

(Neofelis

423 nebulosa) animal number 1 using primers mcb398 and mcb869

425 <400> SEQUENCE: 19

427 tgaatctgag gaggtctctc agtagacaaa gccaccctga cacgattttt cgccttccac

428 ttcacccctcc catattatcat ctcagcctta gcagcagttc accttctatt tctccatgaa

E--> 429 aaggatcca ataaccctc aggaatggta tccgattcag acaaaatccc gttccacccg

60  
120  
(180) counted 179

E--> 430 tactatacaa tcaaagatat cctaggcctc ctagttctaa ttctagecgt cacactactt

E--> 431 gttctattct cccagacct actaggagac cctgacaatt acactcccgc caaccctcta

240  
300  
(328) - found 327

E--> 432 aataccctc cccatatcaa gcctgaat

435 <210> SEQ ID NO: 20

437 <211> LENGTH: (328) - found 327

439 <212> TYPE: DNA

441 <213> ORGANISM: gz22CL

443 <220> FEATURE:

445 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard

(Neofelis

446 nebulosa) animal number 2 using primers mcb398 and mcb869

448 <400> SEQUENCE: 20

450 tgaatctgag gaggcttctc agtagacaaa gccaccctga cacgattttt cgccttccac

60

## RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/821,782B

TIME: 12:08:11

Input Set : A:\0133659 sequence listing.txt

Output Set: N:\CRF4\08082002\I821782B.raw

451 ttcacccctcc catttatcat ctcagcctta gcagcagttc accttctatt tctccatgaa  
 E--> 452 aaggatcca ataaccctc aggaatggta tccgattcag aaaaaatccc gttccaccg  
 E--> 453 tactatacaa tcaaagatat cctaggcctc ctagtcttaa ttctagcgct cacactactt  
 E--> 454 gttctattct cccagacct actaggagac cctgacaatt acactccgc caaccctta  
 E--> 455 aataccctc cccatatcaa gcctgaat  
 1286 <210> SEQ ID NO: (61)  
 1288 <211> LENGTH: 472  
 1290 <212> TYPE: DNA  
 1292 <213> ORGANISM: Balaenoptera edeni  
 E--> 1294 <400> SEQUENCE: (60)  
 1296 taccctgagg acaatatca ttttgaggcg caaccgtcat caccaacctc ttatcagcaa  
 1297 tcccatatcat tggactacc ctagtccaat gaatctggg cggtttctct gtagataaag  
 1298 caacactaac acgtttttt gccctccact ttatcctccc ctccattatt ctaggactag  
 1299 caatggtcca cctcattttc ctccacgaaa caggatccaa taaccccaca ggtattccat  
 1300 ccaacataga caaaatccca ttccaccctc attacacaac taaagacatt ctaggcgccc  
 1301 tactactaat cctaacccta ctaatgctaa ccctattcgt acccgacctt cttggagacc  
 1302 cagacaacta cactccagca aatccactca gtaccccaac acacattaaa ccagaatgat  
 1303 atttctatt tgcatacgca atcctacgat caattcccaa caaattaggc gg  
 E--> 2315 <210> SEQ ID NO: (13)  
 2317 <211> LENGTH: 472  
 2319 <212> TYPE: DNA  
 2321 <213> ORGANISM: Hyperoodon ampullatus  
 E--> 2323 <400> SEQUENCE: (113)  
 2325 taccctgagg acaatatca ttctgaggcg caaccgtcat caccaatctc ctatccgcca  
 2326 ttccctatat cggcactacc ctagtccaat gaatctgagg tggtttctcc gtagacaaaag  
 2327 ccacattaac ccgtttttt gccctccact ttatcctccc attcattatt ctaggccctag  
 2328 caatcgcca cctactattc ctccatgaaa caggatccaa caatcccaca ggaattccat  
 2329 ctgacataga caaaatcccg ttccaccctc actacacaat caaagacact ctaggggccc  
 2330 tattactaat cctagtccca ctacatttaa ccctattcgc acccgacctt ctaggagacc  
 2331 ctgataacta taccacagca aaccactca gactccagc acacatcaaa ccagaatggt  
 2332 acttctatt tgcatacgca atcctacgtt caatccctaa caaactagga gg  
 E--> 2335 <210> SEQ ID NO: (114)  
 4295 <210> SEQ ID NO: (214)  
 4297 <211> LENGTH: (23)  
 4299 <212> TYPE: DNA  
 4301 <213> ORGANISM: Artificial Sequence  
 4303 <220> FEATURE:  
 4305 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b  
 4306 gene of animal species in polymerase chain reaction  
 4308 <400> SEQUENCE: (214)  
 E--> 4310 tagtagaat gaatctgagg agg  
 4313 <210> SEQ ID NO: 215  
 4315 <211> LENGTH: (23)  
 4317 <212> TYPE: DNA  
 4319 <213> ORGANISM: Artificial Sequence  
 4321 <220> FEATURE:  
 4323 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b  
 4324 gene of animal species in polymerase chain reaction  
 4326 <400> SEQUENCE: 215

## RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/821,782B

TIME: 12:08:11

Input Set : A:\0133659 sequence listing.txt

Output Set: N:\CRF4\08082002\I821782B.raw

E--> 4328 atgcaaata ggaagtatca ttc 22  
 4352 <210> SEQ ID NO: 217  
 4354 <211> LENGTH: 472  
 4356 <212> TYPE: DNA  
 4358 <213> ORGANISM: Oreotragus oreotragus  
 4360 <400> SEQUENCE: 217  
 4362 ttccgtgagg acaaatatca ttttgagggg ctacagtcac tactaatctc ctctcagcaa 60  
 4363 ttccatatat tggcacaac ctggtagaat gaatctgagg aggattctcg gtggacaaag 120  
 4364 caacccttac cggattcttt gcctttcact tcactcttcc atttatcatc gcagccctag 180  
 4365 ccatagtaca cctactcttt ctccacgaaa cagggtccaa taacccacaca ggaatctcat 240  
 4366 cagacacaga caaaatccca tttcatcctt attacacaat caaagatatc ctaggcgccc 300  
 4367 tattactaat tctagcttta ttactcttag tattattcac acctgacctc cttggagacc 360  
 4368 cagataacta caccacagca aaccactca acactcccc tcacattaaa ccagaatggt 420  
 E--> 4369 atttctatt ngcatatgca atcctacgat caatcccaa taaactagga gg 472  
 4532 <210> SEQ ID NO: 226  
 4534 <211> LENGTH: 472  
 4536 <212> TYPE: DNA  
 4538 <213> ORGANISM: Bison bonasus  
 4540 <400> SEQUENCE: 226  
 4542 taccatgagg acaaatatca ttttgaggag caacagtcac taccaacctc ctatcagcaa 60  
 4543 tcccatatat cggcacaac ctagtatgaat gaatctgagg cggattctca gtagacaaag 120  
 4544 caacccttac cggatttttc gctttccact ttatcctccc atttattatc atagcaattg 180  
 4545 ccatagttca cctactattc ctccacgaaa cagggtctaa caatccaaca ggaatttctt 240  
 4546 cagacacaga caaaattcca ttccacctt actataccat taaagacatc ctaggagcct 300  
 4547 tattactaat tctaactcta atactactag tactattcgc accggacctc ctcgagacc 360  
 4548 cagataacta caccacagca aatccactta acacacctcc ccacatcaaa cccgaatgat 420  
 E--> 4549 acttcttatt tgcatangca attttacggt caatcccaa caaactagga gg 472  
 4808 <210> SEQ ID NO: 240  
 4810 <211> LENGTH: 472  
 4812 <212> TYPE: DNA  
 4814 <213> ORGANISM: Rupicapra rupicapra  
 4816 <400> SEQUENCE: 240  
 4818 taccatgagg acagatatca ttctggggag caacagttat taccaacctc ctctcagcga 60  
 4819 tcccgatatat tggcacagac ttagtcgaat gaatctgagg aggtctctcg gtagacaagg 120  
 4820 ctaccctcac cggattcttt gccttccact tcactctccc atttatcatt gcagccttag 180  
 4821 ccctagtcca cctactcttc ctccacgaaa caggatctaa caacccacaca ggaatcccat 240  
 E--> 4822 cagatgcgga caaaatccca tttnacccct attataccat caaagacatt ctgggcgcca 300  
 E--> 4823 tactactaat cctcaccctc atactactag tactattnac acctgacctc ctcgagacc 360  
 4824 cagataatta caccacagcg aaccactca acacaccccc tcacattaaa cccgagtgat 420  
 4825 atttcttatt tgcatatgca attctacgat caatcccaa caaacttgga gg 472  
 5111 <210> SEQ ID NO: 255  
 5113 <211> LENGTH: 472  
 5115 <212> TYPE: DNA  
 5117 <213> ORGANISM: Cervus elaphus canadensis  
 E--> 5119 <400> SEQUENCE: AB021096 - must state sequence no. -> should be 255  
 5121 taccatgagg acaaatatca ttctgaggag caacagtcac taccaacctt ctctcagcaa 60  
 5122 ttccatatat tggcacaac ctagtcgaat gggctctgagg aggttttca gtagataaag 120  
 5123 caaccctaac cggattcttc gctttccact ttattctccc atttatcatc gcagcactcg 180  
 5124 ctatagtaca cttactcttc cttcacgaga caggatctaa taacccaaca ggaatcccat 240

## RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/821,782B

TIME: 12:08:11

Input Set : A:\0133659 sequence listing.txt

Output Set: N:\CRF4\08082002\I821782B.raw

5125	cagacgcaga	caaaatcccc	ttccaccott	actatacgat	taaagatatc	ttaggtatct	300
5126	tacttcta	actcttccta	atattactag	tattattcgc	accagatctg	cttggagacc	360
5127	cagacaacta	taccccgca	aatccactca	acacaccccc	tcacattaaa	cctgaatgat	420
5128	atttcctatt	tgcatagca	atcctacgat	caattcccaa	caaactagga	gg	472

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/08/2002  
PATENT APPLICATION:    US/09/821,782B      TIME: 12:08:12

Input Set : A:\0133659 sequence listing.txt  
Output Set: N:\CRF4\08082002\I821782B.raw

Skipped Sequences(NEW RULES):

Sequence(s)\_\_\_missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number

<400> sequence id number

000

Seq#:14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37

Seq#:38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61

Seq#:62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85

Seq#:86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107

Seq#:108,109,110,111,112,113

## VARIABLE LOCATION SUMMARY

DATE: 08/08/2002

PATENT APPLICATION: US/09/821,782B

TIME: 12:08:12

Input Set : A:\0133659 sequence listing.txt

Output Set: N:\CRF4\08082002\I821782B.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:45; N Pos. 269,431

Seq#:216; N Pos. 104,107,128,368,369,431

Seq#:217; N Pos. 425,431

Seq#:226; N Pos. 437

Seq#:240; N Pos. 264,338

Seq#:244; N Pos. 264,265,266,267,268,269,270,271,272,273,274,275,276,277

Seq#:244; N Pos. 278



## VERIFICATION SUMMARY

DATE: 08/08/2002

PATENT APPLICATION: US/09/821,782B

TIME: 12:08:12

Input Set : A:\0133659 sequence listing.txt

Output Set: N:\CRF4\08082002\I821782B.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:25 Counted:26 SEQ:1  
L:32 M:252 E: No. of Seq. differs, <211> LENGTH:Input:25 Found:26 SEQ:1  
L:429 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:19  
M:254 Repeated in SeqNo=19  
L:432 M:252 E: No. of Seq. differs, <211> LENGTH:Input:328 Found:327 SEQ:19  
L:452 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:20  
M:254 Repeated in SeqNo=20  
L:455 M:252 E: No. of Seq. differs, <211> LENGTH:Input:328 Found:327 SEQ:20  
L:971 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:240  
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:420  
L:1294 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:61 differs:60  
L:2315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 13  
L:2323 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:113  
L:2335 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 14 thru 113  
L:4310 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:22 SEQ:214  
L:4328 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:22 SEQ:215  
L:4344 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:216  
L:4344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:216  
L:4344 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:216  
L:4344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:60  
L:4345 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:216  
L:4345 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:216  
L:4345 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:216  
L:4345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:120  
L:4349 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:216  
L:4349 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:216  
L:4349 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:216  
L:4349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:360  
L:4350 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:216  
L:4350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:216  
L:4350 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:216  
L:4350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:420  
L:4369 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:217  
L:4549 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:226  
L:4822 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:240  
M:340 Repeated in SeqNo=240  
L:4897 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:244  
L:4909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:244 after pos.:240  
L:5119 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:255 differs:254